



232367sequence.txt  
SEQUENCE LISTING

<110> KALAJI, MAHER  
WILLIAMS, PETER ANTHONY  
GWENIN, CHRISTOPHER DAVID

<120> IMPROVEMENTS IN AND RELATING TO BIOSENSORS

<130> 31229-232367

<140> 10/582,557

<141> 2006-06-09

<150> PCT/GB2004/004817

<151> 2004-11-17

<150> GB 0328784.4

<151> 2003-12-11

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<170> PatentIn version 3.5

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<211> 654

<212> DNA

<213> Escherichia coli

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<223> K12

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tcgacttcct cgaacctgca agcttggagc gtgctcgccg tgcgggatcg cgagcgtctc      240
gcgaggcttg cccgactgtc cggttaaccag cgccatgtcg agcaggcacc gctgttcctg      300
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cac agc agc ggc ctg gtg ccg cgc ggc agc cat atg gct agc atg act      162
His Ser Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr
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ggt gga cag caa atg ggt cgc gga tcc tgt tgc tgt tgc tgt tgc gat      210
Gly Gly Gln Gln Met Gly Arg Gly Ser Cys Cys Cys Cys Cys Cys Asp
30                               35                               40

atc att tct gtc gcc tta aag cgt cat tcc act aag gca ttt gat gcc      258
Ile Ile Ser Val Ala Leu Lys Arg His Ser Thr Lys Ala Phe Asp Ala
45                               50                               55

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gtg ttc tgt gca aaa acc gcg atg gac gat gtc tgg ctg aag ctg gtt Val Phe Cys Ala Lys Thr Ala Met Asp Asp Val Trp Leu Lys Leu Val 125 130 135			498
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gtc ggt aac ttc ctg ctc ggc gtg gcg gct ctg ggt ctg gac gcg gta Val Gly Asn Phe Leu Leu Gly Val Ala Leu Gly Leu Asp Ala Val 190 195 200			690
ccc atc gaa ggt ttt gac gcc gcc atc ctc gat gca gaa ttt ggt ctg Pro Ile Glu Gly Phe Asp Ala Ala Ile Leu Asp Ala Glu Phe Gly Leu 205 210 215			738
aaa gag aaa ggc tac acc agt ctg gtg gtt gtt ccg gta ggt cat cac Lys Glu Lys Gly Tyr Thr Ser Leu Val Val Val Pro Val Gly His His 220 225 230			786
agc gtt gaa gat ttt aac gct acg ctg ccg aaa tct cgt ctg ccg caa Ser Val Glu Asp Phe Asn Ala Thr Leu Pro Lys Ser Arg Leu Pro Gln 235 240 245			834
aac atc acc tta acc gaa gtg taa ttctctcttg ccgggcatct gcccggtat Asn Ile Thr Leu Thr Glu Val 250 255			888
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Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
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Gly Ser Cys Cys Cys Cys Cys Asp Ile Ile Ser Val Ala Leu Lys  
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Arg His Ser Thr Lys Ala Phe Asp Ala Ser Lys Lys Leu Thr Pro Glu  
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Gln Ala Glu Gln Ile Lys Thr Leu Leu Gln Tyr Ser Pro Ser Ser Thr  
 65 70 75 80

Asn Ser Gln Pro Trp His Phe Ile Val Ala Ser Thr Glu Glu Gly Lys  
 85 90 95

Ala Arg Val Ala Lys Ser Ala Ala Gly Asn Tyr Val Phe Asn Glu Arg  
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Lys Met Leu Asp Ala Ser His Val Val Val Phe Cys Ala Lys Thr Ala  
 115 120 125

Met Asp Asp Val Trp Leu Lys Leu Val Val Asp Gln Glu Asp Ala Asp  
 130 135 140

Gly Arg Phe Ala Thr Pro Glu Ala Lys Ala Ala Asn Asp Lys Gly Arg  
 145 150 155 160

Lys Phe Phe Ala Asp Met His Arg Lys Asp Leu His Asp Asp Ala Glu  
 165 170 175

Trp Met Ala Lys Gln Val Tyr Leu Asn Val Gly Asn Phe Leu Leu Gly  
 180 185 190

Val Ala Ala Leu Gly Leu Asp Ala Val Pro Ile Glu Gly Phe Asp Ala  
 195 200 205

Ala Ile Leu Asp Ala Glu Phe Gly Leu Lys Glu Lys Gly Tyr Thr Ser  
 210 215 220

Leu Val Val Val Pro Val Gly His His Ser Val Glu Asp Phe Asn Ala  
 225 230 235 240

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gtc ggt gtt gta gat gca gct ctg gcc gct cag aac gcc gca cta gct Val Gly Val Val Asp Ala Ala Leu Ala Ala Gln Asn Ala Ala Leu Ala 170 175 180 185	642
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tcc agc cag gcc gtg gaa cgt gta aaa gga gcg gat tca ctg agc gga Ser Ser Gln Ala Val Glu Arg Val Lys Gly Ala Asp Ser Leu Ser Gly 285 290 295	978
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Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
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Gly Ser Cys Cys Cys Cys Cys Cys Ser Leu Gln Asp Glu Ala Leu Lys  
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35

40

45

Ala Trp Gln Ala Arg Tyr Gly Glu Pro Ala Asn Leu Pro Ala Ala Asp  
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Thr Val Ile Ala Gln Met Leu Gln His Arg Ser Val Arg Ala Tyr Ser  
 65 70 75 80

Asp Leu Pro Val Asp Glu Gln Met Leu Ser Trp Ala Ile Ala Ala Ala  
 85 90 95

Gln Ser Ala Ser Thr Ser Ser Asn Leu Gln Ala Trp Ser Val Leu Ala  
 100 105 110

Val Arg Asp Arg Glu Arg Leu Ala Arg Leu Ala Arg Leu Ser Gly Asn  
 115 120 125

Gln Arg His Val Glu Gln Ala Pro Leu Phe Leu Val Trp Leu Val Asp  
 130 135 140

Trp Ser Arg Leu Arg Arg Leu Ala Arg Thr Leu Gln Ala Pro Thr Ala  
 145 150 155 160

Gly Ile Asp Tyr Leu Glu Ser Tyr Thr Val Gly Val Val Asp Ala Ala  
 165 170 175

Leu Ala Ala Gln Asn Ala Ala Leu Ala Phe Glu Ala Gln Gly Leu Gly  
 180 185 190

Ile Val Tyr Ile Gly Gly Met Arg Asn His Pro Glu Ala Met Ser Glu  
 195 200 205

Glu Leu Gly Leu Pro Asn Asp Thr Phe Ala Val Phe Gly Met Cys Val  
 210 215 220

Gly His Pro Asp Pro Ala Gln Pro Ala Glu Ile Lys Pro Arg Leu Ala  
 225 230 235 240

Gln Ser Val Val Leu His Arg Glu Arg Tyr Glu Ala Thr Glu Ala Glu  
 245 250 255

Ala Val Ser Val Ala Ala Tyr Asp Arg Arg Met Ser Asp Phe Gln His  
 260 265 270

Arg Gln Gln Arg Glu Asn Arg Ser Trp Ser Ser Gln Ala Val Glu Arg  
 275 280 285

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42